



DNA sequence:

cccttcattgtctttttagtagaaacccattatctctttcttagggcccaattgaaaacccacattttctttcacctaaccca  
ccaaagccttgacatgttgacgtgaacaccaaactaacacgtgtcatactgccagtgggtatgataaatgctcatacc  
ataccagagtcataagagtttttgggttggtgaaagatttgacggatgccttctctcatttctcaccacactccctccaaa  
cccaacaaaatgtttatattagcaaagccgccaagtgtaaacgaaagtttataaatttcatttctgtgatcttacgta  
attgggaggaagatcaaaattttcaatccccattctctcgattgcttcaattgaagtttctccg

[transit peptide start]

ATGGCGCAAGTTAGCAGAATCTGCAATGGTGTGAGAACCCTCTCTTATCTCCAATCTCTCGAAATCCAGTCAACGCA  
AATCTCCCTTATCGGTTTCTCTGAAGACGCAGCAGCATCCACGAGCTTATCCGATTTCTCGTCTGTTGGGGATTGAAGAA  
GAGTGGGATGACGTTAATTGGCTCTGAGCTTCGTCCTCTTAAGGTCATGTCTTCTGTTTCCACGGCGGAG

[mature peptide starts]

AAAGCGTCGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTCTTATTAAGCTTCTGGCTCCAAGTCTCTATCAA  
ATCGGATCTGCTTCTCGCTGCTCTGTCTGAGGTATATACACTTCGTTTCGTCTTCTCTGTAATCTGAACCTTAGATT  
ATAAAGATTGATACTTTACCATTTTGTCTGTGGTTTATAGGGAACAACCTGTAGTGGACAACCTTGTGAATAGCGATGAC  
ATCAATTACATGCTTGATGCGTTGAAGAGATTGGGACTTAATGTGGAACTGACAGTGAAAATAATCGTGTCTGTAGTTG  
AAGGATGTGCGGGATATTCCAGCTTCCATAGATTCAAAGAGTGATATCGAACTTTACCTCGGTAATGCAGGAACAGC  
AATGCGTCCAATTACCGCTGCGGTCACTGCTGCAGGTGGAAACGCAAGGTAGATTGAAGGAGTTGATGCTTCTTGGTAT  
TTGATGTTTAAAGGAATGGAGCTTTTGTGATGCTTATGATCCATTTATCCAGTTATGTGCTTGATGGGGTGCCCTCGT  
ATGAGAGAAAGACCTATAGGGGATTGGTTGTTGGTCTTAAGCAGCTTGGTGCTGATGTTGAATGTAATCTTGGAACTA  
ACTGCCCTCTGTTTCGTGTCAACGCTAATGGTGGCCTTCCCGGTGGAAAGGTTAGATCTTGCAATGGCATGTGAATAT  
GTAATCTCGTTCCTTACTCTATGAACACTTGCAGAAATGTGTGTTTATCATAGCCTTAGCTTGACAAGATTTTCACTTTT  
TAATCTACTCTCAACGGATGGATCCTAAAATAGAATCGGATTTGGTGATTGGTTTTCTGTTCTCGATTACCGTTTTCTGTT  
GTATGATTTCTTGATTAACAATTAGGAGACATGTTATGCATTTGCAGGTGAAGCTTTCTGGATCAATTAGTAGTCAGTA  
CTTGACTGCTCTGCTCATGTCTGCTCCCTTAGCTCTTGGAGACGTGAGATTGAGATTGTGATAAATTAATTTCTGTT  
CCATATGTTGAAATGACATTGAAGTTGATGGAACGTTTCCGGGTTAGTGTGAGCATAGTGATAGCTGGGATCGTTTCT  
TTGTCAAGGGCGGGCAAAAATACAAGTAGGAGTATTCTTTTCTTCTTCTGAAATCACATCCCTTAGCTTGACAAT  
ATAATGACTAAAAGGTGAATGATTCAAGGTCTCCGGGTAATGCGTATGTAGAAGGTGATGCTTCTAGTGCATGTTATTTT  
TTGGCTGGTGCTGCCATTACCGGTGAACTGTCAAGTCAAGGTTGTGGAACCTACCAGCTTGCAAGGTAATATTTGTAC  
ACTGAATCATCGACGAGGCTGTTAAGTTTATAGTGAAATTCGTCTAGGTCAAAGTTTCTATCTTTGACAAGTTGTATAT  
AACATATTGCAAGATTCTAAGCTCAATTTTTGTGATGAATCTCTAGGGAGATGTAAATTCGCCGAGGTCCTTGAGAA  
AATGGGATGTAAAGTGTCTGGACAGAGAACAGTGTGACTGTGACAGGACCACCTAGAGATGCTTTTGGAAATGAGACAC  
TTGCGGGCTATTGATGTCAACATGAACAAAATGCCTGATGTAGCCATGACCCTTGCCGTGCTTGTCTCTTTGCTGACG  
GTCCAACCACCATAGAGATGGTAAGTAAAAAGCTCTCTCTTATAATTAAGGTTTCTCAATATTCTATGATCACTTAATT  
CTGTTTGGTTAATATAGTGGCTAGCTGGAGAGTAAAGGAGACAGAAAGGATGATTGCCATTTGCACAGAGCTTAGAAAA  
GTAAGAGATTCTTATCTCTCTCTTCTGTCTCTTGACAGTGCTCATTCTAAGTAATTAGCTCATAAATTTGTGTGTTT  
TGTTGAGCTGGGAGCTACAGTGGAAGAAGGTTGAGATTATGTGTGATAACTCCGCCAAAAAGGTGAAAACGGCAGAG  
ATTGATACATATGATGATCATAGAATGGCAATGGCATTCTCTTGCAGCTTGTGCTGATGTTCCAATCACCATCAACG  
ACTCTGGTTGCACAGGAAAACCTTCCCGACTACTTCCAAGTACTTGAAAGAATCACAAGCACTAAacataaactc  
tgttttttcttctgatccaagctt

Fig. 1A



Protein sequence:

MAQVSRICNGVQNP~~SL~~ISNLSKSSQ~~RK~~SP~~LS~~VLKTQHPRAYPISSSWGLKKSGMTLIGSELRLPKVMSSVSTAE  
KASEIVLQPIREISGLIKLP~~GS~~KSL~~SN~~RI~~LL~~LAALSEGTTVDNLLNSDDIN~~YMLD~~ALKRLGLN~~VE~~TDSENNRAVV  
EGCGGIFPASIDS~~KS~~DI~~EL~~YLGNAGTAMP~~PL~~TAAVTAAGNASYVLDGVPRMRERPIGDLVVGLKQLGADV~~ECT~~LG  
TNCPPVRVNANGGLPGGKVKLSGSISSQYLTALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSVEHSD  
SWDRFFVKGQKYKSPGNAYVEGDASSACYFLAGAAITGETTVVEGCGTTS~~LQ~~GDVKFAEVLEKMGCKVSWTENS~~V~~  
TVTGPPRDAFGMRHLRAIDVNNMKMPDVAMTLAVVALFADGPTTIRDVASWRVKETERMIAICTELRKL~~GAT~~VEEG  
SDYCVITPPKKVKTA~~E~~IDTYDDHRMAMAFSLAACADVPI~~T~~INDSGCTRKTFFPDYFQVLERITKH

Fig. 1B



Arabidopsis thaliana wild type sequence:

|          |     |     |     |     |     |     |     |     |     |     |     |
|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Position | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 |
|          | L   | G   | N   | A   | G   | T   | A   | M   | R   | P   | L   |
|          | CTC | GGT | AAT | GCA | GGA | ACA | GCA | ATG | CGT | CCA | CTT |

Arabidopsis thaliana mutant sequences:

|  |     |     |     |     |     |     |     |     |     |     |     |
|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Name   |     |     |     |     |     |     |     |     |     |     |     |
| A <sub>177</sub>                                   | CTC | GGT | AAT | GCA | GCA | ACA | GCA | ATG | CGT | CCA | CTT |
|  | L   | G   | N   | A   | A   | T   | A   | M   | R   | P   | L   |
| I <sub>178</sub>                                   | CTC | GGT | AAT | GCA | GGA | ATA | GCA | ATG | CGT | CCA | CTT |
|  | L   | G   | N   | A   | I   | T   | A   | M   | R   | P   | L   |
| A <sub>177</sub> I <sub>178</sub>                  | CTC | GGT | AAT | GCA | GCA | ATA | GCA | ATG | CGT | CCA | CTT |
|  | L   | G   | N   | A   | A   | I   | A   | M   | R   | P   | L   |
| I <sub>178</sub> S <sub>182</sub>                  | CTC | GGT | AAT | GCA | GGA | ATA | GCA | ATG | CGT | TCA | CTT |
|  | L   | G   | N   | A   | G   | I   | A   | M   | R   | S   | L   |
| A <sub>177</sub> S <sub>182</sub>                  | CTC | GGT | AAT | GCA | GCA | ACA | GCA | ATG | CGT | TCA | CTT |
|  | L   | G   | N   | A   | A   | T   | A   | M   | R   | S   | L   |
| A <sub>177</sub> I <sub>178</sub> S <sub>182</sub> | CTC | GGT | AAT | GCA | GCA | ATA | GCA | ATG | CGT | TCA | CTT |
|  | L   | G   | N   | A   | A   | I   | A   | M   | R   | S   | L   |
| V <sub>178</sub> S <sub>182</sub>                  | CTC | GGT | AAT | GCA | GGA | GTA | GCA | ATG | CGT | TCA | CTT |
|  | L   | G   | N   | A   | G   | V   | A   | M   | R   | S   | L   |
| L <sub>178</sub> S <sub>182</sub>                  | CTC | GGT | AAT | GCA | GGA | TTA | GCA | ATG | CGT | TCA | CTT |
|  | L   | G   | N   | A   | G   | L   | A   | M   | R   | S   | L   |
| A <sub>177</sub> V <sub>178</sub>                  | CTC | GGT | AAT | GCA | GCA | GTA | GCA | ATG | CGT | CCA | CTT |
|  | L   | G   | N   | A   | A   | V   | A   | M   | R   | P   | L   |
| A <sub>177</sub> L <sub>178</sub>                  | CTC | GGT | AAT | GCA | GCA | TTA | GCA | ATG | CGT | CCA | CTT |
|  | L   | G   | N   | A   | A   | L   | A   | M   | R   | P   | L   |

Fig. 2

100  
(1) ATGGCGCAAGTTAGCAGAAATCTGCAATGGTGTGCGAGAACCCAT---CTCTTATCTCAATCTCTCGAATCTCAGTCAACGCAAAATCTCC---CTTATCGG  
(1) ATGGCGCAATCTAGCAGAAATCTGCAATGGTGTGCGAGAACCCATGGTGTATCATCTCAATCTCTCAATCTCTCAATCTCAACCAAAACAAATCACC---TTTCTCCG  
(1) ATGGCACAATTAACAACATGGCTCAAGGGATACAAACCTTA---ATCCCAATCTCAATTTCCATAAACCCCAAGTTCTCTAAATCTTCAAGTTTCTTG  
(1) GCGG-----  
1  
101  
(95) TTTCT---CTGAAGACGAGCAGCATCCAAGAGTTATCCGATTTCGTCTGTGGGATTGAAGAAGAGTGGGATGACGTTAAATTTGGCTCTGAGCTTCG  
(98) TCTCC---TTGAAGACGAGCATCAGC---CTCGAGCTT-----CTTCGTGGGATTGAAGAAGAGTGGAAACGATGCTAAACCGTTCTGTAAATTCG  
(98) TTTTGGATCTAAAAAACTGAAAAATTCAGCAAAAT---CTATGTTGGTTTGAAAAAAGATTCAAATTT---TATGCAAAAGTTTGT  
(5) -----GTCCCGAGG-----  
200  
(95) TTTCT---CTGAAGACGAGCAGCATCCAAGAGTTATCCGATTTCGTCTGTGGGATTGAAGAAGAGTGGGATGACGTTAAATTTGGCTCTGAGCTTCG  
(98) TCTCC---TTGAAGACGAGCATCAGC---CTCGAGCTT-----CTTCGTGGGATTGAAGAAGAGTGGAAACGATGCTAAACCGTTCTGTAAATTCG  
(98) TTTTGGATCTAAAAAACTGAAAAATTCAGCAAAAT---CTATGTTGGTTTGAAAAAAGATTCAAATTT---TATGCAAAAGTTTGT  
(5) -----GTCCCGAGG-----  
300  
(192) TCCTCTTAAGTTCATGTCCTTCTGTTTCCACGGCGGAGAAAGCTCGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTCTTATTAAAGTTCTCTGGC  
(180) CCGGTTAAGTAAACAGCTTCTGTTTCCACGTCGAGAAAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGTTCTCATTAAGTACACCGGA  
(180) TTCCCTTAGGATTTTCAAGATCAGTGGCTACAGCAGAGACCTTCTGAGATAGTGTGCAACCCATTAAGAGATTTCAGGCACCTGTTAAATTTGCCTGGC  
(14) -----AGATCGTGTCTGCGAGGAGATCTCCGGCACCGTCAAGCTGCGGGG  
400  
(292) TCCAGTCTCTATCAAAATCGGATCCTGCTTCTCGTCTGTGAGGAAACAACTGTAGTGAACAACTTGTGAATAGCGATGACATCAATATACATGC  
(280) TCCAAATCTCTCAATCGGATCCTCTTCTGCGCTCTATCTGAGGAACTACTGTAGTGAACAACTTGTGAACAGTGTGATGACATCAACTACATGC  
(280) TCTAAATCAATATCTAATAGAAATCTCTTCTGCTGCTTATCTGAAGAAACAACTGTGTTGAACAACTTGAAGTGTGATGATTCATTAATCATGC  
(67) TCCAGTGTGCTTTCCAAACCGGATCCTCTACTGCGCCCTGTCGAGGGGACAACTGTGTTGATTAACCTGTGAACAGTGAAGATGTCCACTACATGC  
500  
(392) TTGATGCGTTGAAGAGATTGGGACTTAATGTGAAACGTGACAGTGAATAATCGTGTGTAGTTGAAGATGTGGGGGATATCCAGCTTCCATAGA  
(380) TTGATGCGTTGAAGAGTTGGGCTTAAACGTGAAACGTGACAGTGAATAACCAACCGTGGTGTGAAGATGCGGTGAATAATCCAGCTTCCCTAGA  
(380) TTGATGCGTTGAAACCACTTGGACTGCACTGAGAGAGATAGTGAACCAACCAACGAGTGTGTTGAAGTGTGTTGGGCTTTTCCCTGTTGTAAGA  
(167) TCGGGCTTGAAGACTCTTGGTCTCTCTGTGAAAGCGGACAAAGCTGCCAAAGAGCTGTAGTTGTTGGCTGTGGTGAAGATTCACAGTTG---AGGA  
600  
(492) TTCAAAGAGTGATATCGAACTTTACCTCGGTAATGCAGGAAACAGCAATGCGTCCACTTACCCTGCGGTCACTGTGCGAGTGGAAACGCAAGTTATGTG  
(480) TTCAAAGAGTGATATCGAACTTTACCTCGGTAATGCAGGAAACAGCAATGCGTCCACTTACCCTGCGGTCACTGTGCGAGTGGAAACGCAAGTTATGTG  
(480) GTCAAAGGAGAAATTAACCTGTTCTTGGAAATGCAGGAAACAGCAATGCGGCCCACTAACAGCAGCAGTTACTGTAGCTGGTGGAAATTCAGAGTATGTA  
(264) TGCTAAAGAGGAGTGAGCTCTTCTTGGGGAATGCTGAACTGCAATGCGGCCCACTGAACAGCAGCTGTACTGTCTGTGGTGGAAATGCAACTTACGTG

Fig. 3A



|                 |      |  |
|-----------------|------|--|
|                 | 700  |  |
| atepspscDNA.seq | 601  | (592) CTTGATGGGTGCTCGTATGAGAGAAAGACCTATAGGGGATTTGGTTGGTCTTAAGCAGCTTGGTCTGATGTTGAATGTA                      |
| bnepsdcna.seq   |      | (580) CTTGATGGGTGCTCGTATGAGAGAAAGACCTATAGGGGATTTGGTTGGTCTTAAGCAGCTTGGTCTGATGTTGAATGTA                      |
| petaroacdna.seq |      | (580) CTTGATGGGTGCTCGTATGAGAGAGAGACCAATTAAGTGTGTTGGTCTTAAGCAGCTTGGTCTGATGTTGAATGTA                         |
| zmepsps.seq     |      | (364) CTTGATGGGTGCTCGTATGAGAGAGAGACCAATTAAGTGTGTTGGTCTTAAGCAGCTTGGTCTGATGTTGAATGTA                         |
| atepspscDNA.seq | 800  | (692) GCCCTCCTGTTGGTCAACCGTAAATGGTGGCCTTCCGGTGGAAAGGTGAAGCTTCTGGATCAATTAAGTCTGATGTTGAATGTA                 |
| bnepsdcna.seq   |      | (680) GTCCCTCCTGTTGGTCAACCGTAAATGGTGGCCTTCCGGTGGAAAGGTGAAGCTTCTGGATCAATTAAGTCTGATGTTGAATGTA                |
| petaroacdna.seq |      | (680) GTCCCTCCTGTTGGTCAACCGTAAATGGTGGCCTTCCGGTGGAAAGGTGAAGCTTCTGGATCAATTAAGTCTGATGTTGAATGTA                |
| zmepsps.seq     |      | (464) GCCCACCTGTTGGTCAACCGTAAATGGTGGCCTTCCGGTGGAAAGGTGAAGCTTCTGGATCAATTAAGTCTGATGTTGAATGTA                 |
| atepspscDNA.seq | 900  | (792) TGCTCCCTTAGCTCTTGGAGACGTGAGATTGAGATTGCTCGATAAATTAATTTCTGTTCCATATGTTGAATGACATTTGAATGTA                |
| bnepsdcna.seq   |      | (780) AGCTCCTTAGCTCTTGGAGACGTGAGATTGAGATTGCTCGATAAATTAATTTCTGTTCCATATGTTGAATGACATTTGAATGTA                 |
| petaroacdna.seq |      | (780) TGCTCCCTTAGCTCTTGGAGATTGAGATTGAGATTGCTCGATAAATTAATTTCTGTTCCATATGTTGAATGACATTTGAATGTA                 |
| zmepsps.seq     |      | (564) TGCTCCTTTGGCTCTTGGGGATGAGATTGAAATCAATGATAAATTAATCTCCATTCGATCGTGAATGACATTTGAATGTA                     |
| atepspscDNA.seq | 1000 | (892) GTTAGTGTGAGCATAGTATAGTGGGATCGTTTCTTGTCAAGGGCGGCAAAATACAAGTCTCCGGTAAATGCGTATGTAAGGTGATGCTTCTA         |
| bnepsdcna.seq   |      | (880) GTTAGTGTGAGCATAGTATAGTGGGATCGTTTCTTGTCAAGGGCGGCAAAATACAAGTCTCCGGTAAATGCGTATGTAAGGTGATGCTTCTA         |
| petaroacdna.seq |      | (880) ATTTCTGTGGAGCACAGTATAGTGGGACAGGTTCTTTGTCCGAGGAGGTGAGAAATACAAGTCTCCGGTAAATGCGTATGTAAGGTGATGCTTCTA     |
| zmepsps.seq     |      | (664) GTGAAAGCAGAGCATTTCTGATAGTGGGACAGATTCTACATTAGGGGAGGTCAAAATACAAGTCTCCGGTAAATGCGTATGTAAGGTGATGCTTCTA    |
| atepspscDNA.seq | 1100 | (992) GTGCATGTTATTTCTTGGCTGGTGTGCCATTACCGGTGAAACTCTCACAGTCTGAGGTTGTGAACTACAGCTTGCAGGGAGATGTAAGTTCGCGCA     |
| bnepsdcna.seq   |      | (980) GTGCATGTTATTTCTTGGCTGGTGTGCCATTACCGGTGAAACTCTCTCGAAGTTGTGAACTACAGCTTGCAGGGAGATGTAAGTTCGCGCA          |
| petaroacdna.seq |      | (980) GTGCATGTTATTTCTTGGCTGGTGTGCCATTACCGGTGAAACTCTCTCGAAGTTGTGAACTACAGCTTGCAGGGAGATGTAAGTTCGCGCA          |
| zmepsps.seq     |      | (764) GCGCAAGCTATTTCTTGGCTGGTGTGCCATTACCGGTGAAACTCTCTCGAAGTTGTGAACTACAGCTTGCAGGGAGATGTAAGTTCGCGCA          |
| atepspscDNA.seq | 1200 | (1092) GGTCTTGTGAGAAATGGGATGTAAGTGTCTGTGACAGAGAACAGTGTGATGTCAGAGACCACTAGAGATGCTTTTGGAAATGAGACACTTGGGGCT    |
| bnepsdcna.seq   |      | (1080) GGTCTTGTGAGAAATGGGATGTAAGTGTCTGTGACAGAGAACAGTGTGATGTCAGAGACCACTAGAGATGCTTTTGGAAATGAGACACTTGGGGCT    |
| petaroacdna.seq |      | (1080) GGTACTTGAAATGGGAGCTGAAGTGTACGTGTGACAGAGAACAGTGTGATGTCAGAGACCACTAGAGATGCTTTTGGAAATGAGACACTTGGGGCT    |
| zmepsps.seq     |      | (864) GGTACTTGAGATGATGGGAGCGAAGTGTACATGAGCCGAGACTAGGTAACTGTTACTTGGCCCACTCGGGAGGCCATTTGGGAGGAAACACCTCAAGGCG |

Fig. 3B



1201  
(1192) atepspscDNA.seq  
(1180) bnepscDNA.seq  
(1180) petaroacDNA.seq  
(964) zmepps.seq  
1300  
(1292) atepspscDNA.seq  
(1280) bnepscDNA.seq  
(1280) petaroacDNA.seq  
(1064) zmepps.seq  
1401  
(1392) atepspscDNA.seq  
(1380) bnepscDNA.seq  
(1380) petaroacDNA.seq  
(1164) zmepps.seq  
1501  
(1492) atepspscDNA.seq  
(1480) bnepscDNA.seq  
(1480) petaroacDNA.seq  
(1264) zmepps.seq  
1572

Fig. 3C

|     |       |   |     |
|-----|-------|---|-----|
| 1   | (1)   | MAQVSRICNGVQNP-SLISNLSKSSQKSPLSVSLKTKQHPRAYPISSSWGKKSGMTLIGSELR-----PLKVMSSSVSTA EKASEIVLQPIREISGLI   | 100 |
|     | (1)   | MAQSSRICHGVPNCVILNLSKSNQKSPFVSLKTHQ-----PRASSWGLKKS GMTLNGSVIR-----PVKVTASVSTSEKASEIVLQPIREISGLI      |     |
|     | (1)   | MAQINNMAQGIQTL-NPNSNFHKPQVPKSSFLVFGSKK-----LKNSA-----NSMLVLKDSIFWQKFCSPRISASVATAQKPFSEIVLQPIKEISGTV   |     |
|     | (1)   | AG-----AEEIVLQPIKEISGTV   |     |
| 101 | (94)  | KLPGSKSLSNRIILLAAALSEGTTVDNLLNSDDINMYLDALKRLGLNVETDSENNRAVVEGCGGIFPASIDSKSDIELYLGNAGTAMRPLTAATAAAGN   | 200 |
|     | (90)  | KLPGSKSLSNRIILLAAALSEGTTVDNLLNSDDINMYLDALKRLGLNVETDSENNRAVVEGCGGIFPASIDSKSDIELYLGNAGTAMRPLTAATAAAGN   |     |
|     | (90)  | KLPGSKSLSNRIILLAAALSEGTTVDNLLNSDDIHYMLGALKTLGLHVEEDSANQRAVVEGCGGLFPVGKESKEEIQFLGNAGTAMRPLTAATAVTAAGN  |     |
|     | (19)  | KLPGSKSLSNRIILLAAALSEGTTVDNLLNSDEVDHYMLGALRTLGLSVEADKAAKRAVVVCGGKFPV-EDAKEEVQLFLGNAGTAMRPLTAATAAAGN   |     |
| 201 | (194) | ASYVLGDGVPRMREPIGDLVVGLKQLGADVECTLGTNCPPVRNVNANGGLPGGKVKLSGSISSQYLTALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLM | 300 |
|     | (190) | ASYVLGDGVPRMREPIGDLVVGLKQLGADVECTLGTNCPPVRNVNANGGLPGGKVKLSGSISSQYLTALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLM |     |
|     | (190) | ASYVLGDGVPRMREPISDLVDGLKQLGAEVDCLGTCKPPVRIIVSKGGLPGGKVKLSGSISSQYLTALLMAAPLALGDVEIEIIDKLISVPYVEMTLKLM  |     |
|     | (118) | ATYVLGDGVPRMREPIGDLVVGLKQLGADVDCLGTDCPPVRNVNGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIEIIDKLISIPYVEMTLRLM  |     |
| 301 | (294) | ERFGYSVEHSDSWDRFFVKGGQKYKSPGNAVVEGDASSACYFLAGAAITGETVTVEGCGTTSLQGDVKFAEVLKMGCKVSWTENSVTVTGPPRDAFGMR   | 400 |
|     | (290) | ERFGYSAEHSDSWDRFFVKGGQKYKSPGNAVVEGDASSASYFLAGAAITGETVTVEGCGTTSLQGDVKFAEVLKMGCKVSWTENSVTVTGPPRDAFGMR   |     |
|     | (290) | ERFGISVEHSSWD RFFVRGGQKYKSPGKAFVEGDASSASYFLAGAAVTGGTITVEGCGTNSLQGDVKFAEVLKMGAEVTTWTE NSVTVTGPPRSSSGRK |     |
|     | (218) | ERFGVKAHSDSWDRFFYIKGGQKYKSPKNAVVEGDASSASYFLAGAAITGGTITVEGCGTTSLQGDVKFAEVLMMGAKVTWTETSVTVTGPPREPFGKR   |     |
| 401 | (394) | HLRAIDVNMNMKPDVAMTLAVVALFADGPTTIRDVASWRVKETERMIAICTELRKLGAATVEEGSDYCVITPPKKVKTAETIDYDDHRMAMAFSLAACADV | 500 |
|     | (390) | HLRAVDNMNMKPDVAMTLAVVALFADGPTTIRDVASWRVKETERMIAICTELRKLGAATVEEGSDYCVITPPAKVKPAETIDYDDHRMAMAFSLAACADV  |     |
|     | (390) | HLRAIDVNMNMKPDVAMTLAVVALYADGPTAIRDVASWRVKETERMIAICTELRKLGAATVEEGPDYCIITPPEKLNVTIDYDDHRMAMAFSLAACADV   |     |
|     | (318) | HLKAIDVNMNMKPDVAMTLAVVALFADGPTAIRDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVTIDYDDHRMAMAFSLAACAEV    |     |
| 501 | (494) | PVTINDSGCTRKTFFPDYFQVLERITKH  | 527 |
|     | (490) | PVTIKDPGCTRKTFFPDYFQVLESITKH  |     |
|     | (490) | PVTINDPGCTRKTFFPNYFDVLQQYSKH  |     |
|     | (418) | PVTIRDPGCTRKTFFPDYFDVLSTFVKN  |     |

Fig. 4